ABSTRACT OF THE INVENTION

A method of determining the clinical outcome of a subject with a cancer using a Genomic Damage Fraction comprising, (a) determining the relative change in quantity of nucleic acids between cancerous cells and non-cancerous cells of said subject, (b) determining the Genomic Damage Fraction from the results of step (a), and (c) determining the prognosis of said subject according to said subject's GDF, where a GDF greater than a predetermined GDF is indicative of a first clinical outcome (e.g., a poor prognosis), and a GDF lesser than a predetermined GDF is indicative of a second clinical outcome (e.g., a good prognosis); and a method of identifying certain genomic sequences whose alterations during tumorigenesis of a subject with a cancer have prognostic value for determining the clinical outcome of said subject comprising, (a) determining the molecular profiles of genomic losses and gains ("amplotyping") of tumors at different stages of progression from the same cancer patient, (b) identifying changes (losses and gains) specifically associated to the more advanced stages of tumor progression (e.g., metastatic stage), and (c) determining the prognosis of said subject according to said subject's status of these genomic sequences of step b, where a change (loss or gain) is indicative of a first clinical outcome (i.e., poor prognosis), and no change (i.e., no loss or gain) is indicative of a second clinical outcome (i.e., good prognosis).